

In the Claims

1. (currently amended) A method of predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with an anti-proliferative therapy, said method comprising:

(a) obtaining an expression profile for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 for a response to said anti-proliferative therapy in a sample from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to predict whether said subject is susceptible to undesirable toxicity.

2. (original) The method according to Claim 1, wherein said anti-proliferative therapy comprises administration of ionizing radiation.

3. (original) The method according to Claim 1, wherein said anti-proliferative therapy comprises administration of a chemotherapeutic agent that results in DNA damage.

4. (original) The method according to Claim 3, wherein said DNA damage comprises double-stranded breaks in DNA.

5. (currently amended) A method of determining whether a subject is susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining an expression profile for the response to radiation for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine whether said subject is susceptible to undesirable radiation toxicity.

6. (original) The method according to Claim 5, wherein expression profile is a transcriptional profile.

7. (canceled)

8. (currently amended) The method according to Claim 5, wherein said expression profile comprises at least ~~50~~ 25 sequences ~~from Table 3~~ selected from the 50 top ranked genes set forth in Table 3.

9. (original) The method according to Claim 5, wherein said undesirable toxicity is at least a grade 2 toxicity.

10. (currently amended) A method of determining whether a subject is susceptible to undesirable toxicity resulting from treatment with administration of a chemotherapeutic agent that induces double-stranded breaks in DNA, said method comprising:

(a) obtaining an expression profile for the response to said chemotherapeutic agent for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine whether said subject is susceptible to undesirable toxicity.

11. (currently amended) A method of predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining an expression profile for the response to radiation for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said subject is susceptible to undesirable radiation toxicity.

12. (original) The method according to Claim 11, wherein expression profile is a transcriptional profile.

13. (canceled)

14. (currently amended) The method according to Claim 11, wherein said expression profile comprises at least ~~50~~ 25 sequences ~~from Table 3~~ selected from the 50 top ranked genes set forth in Table 3.

15. (original) The method according to Claim 11, wherein said undesirable toxicity is at least a grade 2 toxicity.

16. (canceled)

17. (currently amended) A method of determining the suitability of a patient for radiation therapy, the method comprising:

predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining an expression profile for the response to radiation for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said patient is susceptible to undesirable radiation toxicity;

wherein a patient that is predicted to have a high probability of undesirable radiation toxicity is less suitable for radiation therapy.

18. (original) The method according to Claim 17, wherein expression profile is a transcriptional profile.

19. (canceled)

20. (currently amended) The method according to Claim 17, wherein said expression profile comprises at least ~~50~~ 25 sequences ~~from Table 3~~ selected from the 50 top ranked genes set forth in Table 3.

21. (original) The method according to Claim 17, wherein said undesirable toxicity is at least a grade 2 toxicity.

22. (currently amended) A method of determining the suitability of a patient for treatment with an anti-proliferative chemotherapeutic agent that induces double-stranded breaks in DNA, the method comprising:

predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with said chemotherapeutic agent, said method comprising:

(a) obtaining an expression profile for the response to said chemotherapeutic agent for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said patient is susceptible to undesirable toxicity;

wherein a patient that is predicted to have a high probability of undesirable toxicity is less suitable for said treatment with an anti-proliferative chemotherapeutic agent.

23. (currently amended) A method of optimizing anti-proliferative therapy for a patient, the method comprising:

(a) obtaining an expression profile for the response to said anti-proliferative therapy for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said patient is susceptible to undesirable toxicity;

wherein a dose of said anti-proliferative therapy is selected to minimize to undesirable toxicity, while providing for effective anti-proliferative activity.

24. (original) The method according to Claim 23, further comprising obtaining an expression profile for a response to one or more additional anti-proliferative therapies;

comparing said expression profiles to determine which therapy minimizes undesirable toxicity while providing for effective anti-proliferative activity.

25. (currently amended) The method according to Claim 23, further comprising obtaining an expression profile for the response to said anti-proliferative therapy for (i) a normal cell sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject and (ii) a tumor cell sample ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject;

comparing said expression profiles from said normal cell and said tumor cell to determine which therapy minimizes undesirable toxicity while providing for effective anti-proliferative activity.

26. (currently amended) A method of obtaining an expression profile for the transcriptional response to radiation, the method comprising:

- exposing a cell sample from an individual to radiation;
- extracting mRNA from said cell;
- quantitating the level of mRNA corresponding to ~~a sequence in Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3;
- comparing said level of mRNA to the level of said mRNA present in a cell sample from said individual not exposed to radiation.

27. (original) The method according to Claim 26, wherein said exposing to radiation comprises exposes said cell to a dose of ionizing radiation of from about 2 to about 10 Gy.

28. (original) The method according to Claim 27, wherein said mRNA is extracted after at least about 2 and not more than about 24 hours following said exposure.

29. (original) The method according to Claim 27, further comprising exposing a cell sample from said individual to ultraviolet radiation at a dose of at least about 5 J/m<sup>2</sup> and not more than about 50 J/m<sup>2</sup>.

30. (original) The method according to Claim 29, wherein said mRNA is extracted after at least about 4 and not more than about 72 hours following said exposure.

31. (original) The method according to Claim 26, wherein said comparing step comprises a nearest shrunken centroid analysis step.

32. (original) A method of obtaining an expression profile for the transcriptional response in a phenotype of interest, the method comprising:

- exposing a cell sample from an individual to said anti-proliferative therapy;
- extracting mRNA from said cell;
- quantitating the level of mRNA corresponding to a sequence of interest;
- comparing by nearest shrunken centroid analysis said level of mRNA to the level of said mRNA present in a cell sample from said individual not exposed to said anti-proliferative therapy.

33. (original) The method according to Claim 32, wherein said phenotype of interest comprises anti-proliferative therapy.

34-46 (canceled)